

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by ≥ 2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-11 03:00:14. Filters applied: disease name contains "HAVCR2-related cancer predisposition" (4 matching pairs). · Rows: 4 · Generated: 2026-10-11 07:47:59

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Alzheimer disease	HAVCR2-related cancer predisposition	1	1	HAVCR2 (2)	0.00045	1.00000	1.440e-1	1.450e-1	
HAVCR2-related cancer predisposition	Oligodendroglioma	1	1	HAVCR2 (2)	0.00179	1.00000	3.630e-2	3.832e-2	
HAVCR2-related cancer predisposition	Lewy body disease	1	1	HAVCR2 (2)	0.01042	1.00000	6.170e-3	7.415e-3	
HAVCR2-related cancer predisposition	Hemophagocytic lymphohistiocytosis	1	1	HAVCR2 (3)	0.11111	1.00000	5.195e-4	1.061e-3	